containing all possible base sequences of that predetermined length and the

base sequences being incapable of ligating to each other; and

(b) a means for resolving a measured quantity of a hybridized probe into

quantities which correspond to unique amounts of the templates to which the

probe hybridizes.

36.   (Amended) A kit according to claim 33, wherein the base sequence of each

probe is unphosphorylated at both [31] 3' and [51] 5' ends.

Kindly add new claims 41-43.

41.   A method of using the kit of claim 33 comprising:

(a)   contacting a target DNA population with the array of hybridization

probes;

(b)   cleaving the labels from hybridized probes to identify the hybridized

probes; and

(c)   determining the sequence of the DNA from the identity of the

hybridized probes.

42.   A kit according to claim 33, wherein the means comprises an algorithm.

43.   A kit according to claim 33, wherein the means comprises a computer

program.